SEQUENCE LISTING

<110> Seoul National University Industry Foundation

<120> ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT

<130> 20020-02USA

<140> US 10/660,499
<141> 2003-09-12

<150> KR 2003-19069
<151> 2003-03-27

<160> 9

<170> KopatentIn 1.71

<210> 1
<211> 1089
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (52)..(816)
<223> Glycine max expansin (GmEXP1)

<400> 1
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atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt 99
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
1 5 10 15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
20 25 30
cat gcc act ttt tat ggg ggt agt gat gct tca gga act atg ggg gga 195
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
35 40 45
gct tgt ggg tat ggg aat ctg tat gca act ggg tat gga act aga act 243
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
50 55 60
gca gct tta agc act gcc tta ttt aat gat gga gct tcc tgt ggt cag 291
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
65 70 75 80
tgc tac aaa att ata tgt gat tac aaa tca gac tct aga tgg tgc atc 339
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile

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                85                  90                  95
aaa gga aga tct  gta acc gta  act gcc aca aac  ttt  tgc cct  ccc aat   387
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
            100                 105                 110
ttc  gcc ctt  cct  aac aac aat  gga ggc tgg tgc aac  cca cca ctc  aag 435
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
        115                 120                 125
cat ttt  gat  atg gcc caa ccc gct tgg gaa aag att ggt att tac aga      483
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
    130                 135                 140
gga ggg atc gtc ccc gtg cta  ttt caa  agg gtt cca tgc  aaa aag cat      531
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
145                 150                 155                 160
gga ggg gtt agg  ttc agt  gtg aat ggg agg gac  tac ttt  gag cta  gta   579
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
                165                 170                 175
ttg atc agc aat  gtg ggg ggt gct gga tcc atc caa tca gtg  ttc att      627
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
            180                 185                 190
aaa ggc tca aaa  act gga tgg atg  gca atg  tca aga aat  tgg ggt tct   675
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
        195                 200                 205
aat  tgg caa tcc  aat gcg tat  ttg  aat  ggt caa tct  ttg  tcc ttc  agg  723
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
    210                 215                 220
gtc acc  acc act  gat gga gag acc aga gtt  ttc  caa gat att gtt cca    771
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
225                 230                 235                 240
gta agt  tgg aca ttc  ggc caa act  ttc  tct agc cca  gtt cag ttc  taag  820
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
                245                 250                 255
ctgattacag ataaaccaac caacggctga ggcgtgcttt tttattttat tactggagct      880
gcccgccacc cttcttctgg ttttgattat tcccatcaac tccaagccct ctatcaaggc      940
ataaattctt atcaataata caatcaatca ccatcatatc atcataagct tgtatatcaa     1000
ataaacatct ttcaagttta aattaattta tactataaat tgttgtaata tcattatagt     1060
tgaagttcaa aaaaaaaaaa aaaaaaaaa                                       1089


<210>  2
<211>  255
<212>  PRT
<213>  Glycine max

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His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
        35                  40                  45
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Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
50 55 60
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
65 70 75 80
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
85 90 95
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
100 105 110
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
115 120 125
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
130 135 140
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
145 150 155 160
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
165 170 175
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
180 185 190
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
195 200 205
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
210 215 220
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
225 230 235 240
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
245 250 255

<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3
nnggatccga ygcntcnggn acnatgggyg gygctgygyt angg 44

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
nnggatcctt kswytgccar ttnnsncccc arttnck 37

<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 5
gaygcnwsng gnacnatggg nggngcntgy ggntayggna ayytntaygc nacnggntay 60
ggnacnmgna cngcngcnyt nwsnacngcn ytnttyaayg ayggngcnws ntgyggncar 120
tgytayaara thathtgyga ytayaarwsn gaywsnmgnt ggtgyathaa rggnmgnwsn 180
gtnacngtna cngcnacnaa yttytgyccn ccnaayttyg cnytnccnaa yaayaayggn 240
ggntggtgya ayccnccnyt naarcaytty gayatggcnc arccngcntg ggaraarath 300
ggnathtaym gnggnggnat hgtnccngtn ytnttycarm gngtnccntg yaaraarcay 360
ggnggngtnm gnttywsngt naayggnmgn gaytayttyg arytngtnyt nathwsnaay 420
gtnggnggng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg 480
gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay 519

<210> 6
<211> 269
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe (antisense)

<400> 6
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gaacugggcu agagaaaguu uggccgaaug uccaacuuac uggaacaaua ucuuggaaaa 120
cucuggucuc uccaucagug guggugaccc ugaaggacaa agauugacca uucaaauacg 180
cauuggauug ccaauuagaa ccccaauuuc uugacauugc cauccaucca guuuuugagc 240
cuuuaaugaa cacugauugg auggaucca 269

<210> 7
<211> 389
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe (sense)

<400> 7
uggauccauc caaucagugu ucauuaaagg cucaaaaacu ggauggaugg caaugucaag 60
aaauuggggu ucuaauuggc aauccaaugc guauuugaau ggucaaucuu uguccuucag 120
ggucaccacc acugauggag agaccagagu uuuccaagau auuguuccag uaaguuggac 180
auucggccaa acuuucucua gcccaguuca guucuaagcu gauuacagau aaaccaacca 240
acggcugagg cgugcuuuuu uauuuuauua cuggagcugc ccgccacccu ucuucugguu300
uugauuauuc ccaucaacuc caagcccucu aucaaggcau aaauucuuau caauaauaca 360
aucaaucacc aucauaucau cauaagcuu 389

<210> 8
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
accaagcttc aacctctcat cattaggc 28

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
accaagcttg gagttgatgg gaataatca 29